

600-1-200

(Sheet 1 of 15)

CAG ATG GAT CCT AAT AGA ATA TCA GAA GAT GGC ACT CAC TGC ATT TAT Gln Met Asp Pro Asn Arg Ile Ser Glu Asp Gly Thr His Cys Ile Tyr 1 5 10 15	48
AGA ATT TTG AGA CTC CAT GAA AAT GCA GAT TTT CAA GAC ACA ACT CTG Arg Ile Leu Arg Leu His Glu Asn Ala Asp Phe Gln Asp Thr Thr Leu 20 25 30	96
GAG AGT CAA GAT ACA AAA TTA ATA CCT GAT TCA TGT AGG AGA ATT AAA Glu Ser Gln Asp Thr Lys Leu Ile Pro Asp Ser Cys Arg Arg Ile Lys 35 40 45	144
CAG GCC TTT CAA GGA GCT GTG CAA AAG GAA TTA CAA CAT ATC GTT GGA Gln Ala Phe Gln Gly Ala Val Gln Lys Glu Leu Gln His Ile Val Gly 50 55 60	192
TCA CAG CAC ATC AGA GCA GAG AAA GCG ATG GTG GAT GGC TCA TGG TTA Ser Gln His Ile Arg Ala Glu Lys Ala Met Val Asp Gly Ser Trp Leu 65 70 75 80	240
GAT CTG GCC AAG AGG AGC AAG CTT GAA GCT CAG CCT TTT GCT CAT CTC Asp Leu Ala Lys Arg Ser Lys Leu Glu Ala Gln Pro Phe Ala His Leu 85 90 95	288
ACT ATT AAT GCC ACC GAC ATC CCA TCT GGT TCC CAT AAA GTG AGT CTG Thr Ile Asn Ala Thr Asp Ile Pro Ser Gly Ser His Lys Val Ser Leu 100 105 110	336
TCC TCT TGG TAC CAT GAT CGG GGG TGG GGT AAG ATC TCC AAC ATG ACT Ser Ser Trp Tyr His Asp Arg Gly Trp Gly Lys Ile Ser Asn Met Thr 115 120 125	384
TTT AGC AAT GGA AAA CTA ATA GTT AAT CAG GAT GGC TTT TAT TAC CTG Phe Ser Asn Gly Lys Leu Ile Val Asn Gln Asp Gly Phe Tyr Tyr Leu 130 135 140	432
TAT GCC AAC ATT TGC TTT CGA CAT CAT GAA ACT TCA GGA GAC CTA GCT Tyr Ala Asn Ile Cys Phe Arg His His Glu Thr Ser Gly Asp Leu Ala 145 150 155 160	480
ACA GAG TAT CTT CAA CTA ATG GTG TAC GTC ACT AAA ACC AGC ATC AAA Thr Glu Tyr Leu Gln Leu Met Val Tyr Val Thr Lys Thr Ser Ile Lys 165 170 175	528
ATC CCA AGT TCT CAT ACC CTG ATG AAA GGA GGA ACC ACC AAG TAT TGG Ile Pro Ser Ser His Thr Leu Met Lys Gly Gly Ser Thr Lys Tyr Trp 180 185 190	576
TCA GGG AAT TCT GAA TTC CAT TTT TAT TCC ATA AAC GTT GGT GGA TTT Ser Gly Asn Ser Glu Phe His Phe Tyr Ser Ile Asn Val Gly Gly Phe 195 200 205	624
TTT AAG TTA CGG TCT GGA GAG GAA ATC AGC ATC GAG GTC TCC AAC CCC Phe Lys Leu Arg Ser Gly Glu Glu Ile Ser Ile Glu Val Ser Asn Pro 210 215 220	672
TCC TTA CTG GAT CCG GAT CAG GAT GCA ACA TAC TTT GGG GCT TTT AAA Ser Leu Leu Asp Pro Asp Gln Asp Ala Thr Tyr Phe Gly Ala Phe Lys 225 230 235 240	720

Figure 1

GTT CGA GAT ATA GAT TGA GCCCCAGTTT TTGGAGTGT TATGTATTTCC	768
Val Arg Asp Ile Asp *	
245	
TGGATGTTG GAAACATTTT TTAAAACAAG CCAAGAAAAGA TGTATATAGG TGTGTGAGAC	828
TACTAAGAGG CATGGCCCAA CGGTACACGA CTCAGTATCC ATGCTCTTGA CCTMTGTAGAG	888
AACACCGGTA TTTACAGCCA GTGGGAGATG TTAGACTCAT GGTGTGTTAC ACAATGGTTT	948
TTAAATTTG TAATGAATTTC CTAGAATTAA ACCAGATTGG AGCAATTACG GGTTGACCTT	1008
ATGAGAAAAT GCATGTGGC TATGGGAGGG GTTGGTCCCT GGTCAATGTGC CCCTTCGAG	1068
CTGAAGTGGG GAGGGTGTCA TCTAGGCCAA TTGAAGGATC ATCTGAAGGG GCAAATTCTT	1128
TTGAATTGTT ACATCATGCT GGAACCTGCA AAAAATACCTT TTTCTAATGA GGAGAGAAAA	1188
TATATGTATT TTTATATAAT ATCTAAAGTT ATATTTCAGA TGTAATGTTT TCTTTGCAAA	1248
GTATTGTAATTTTGT GCTATAGTAT TTGATTCAGA ATATTTAAAAA ATGTCCTGCT	1308
GTGACATAT TTAATGTTTT AAATGTACAG ACATATTTAA CTGGTGCAC TTGTAATTC	1368
CCTGGGGAAA ACTTGCAGCT AAGGAGGGGA AAAAATGTTG TTTCTTAATA TCAAATGCAG	1428
TATATTTCTT CGTTCTTTTT AAGTTAATAG ATTTTTTCAG ACTTGTCAAG CCTGTGCAAA	1488
AAAATTTAAA TGGATGCCTT GAATAATAAG CAGGATGTTG GCCACCAGGT GCCTTTCAAA	1548
TTTAGAAAATC AATTGACTTT AGAAAGCTGA CATTGCCAAA AAGGATACAT AATGGGCCAC	1608
TGAAATCTGT CAAGAGTAGT TATATAATTG TTGAACAGGT GTTTTCCAC AAGTGCCGCA	1668
AATTGTACCT TTTTTGTTT TTTTCAAAAT AGAAAAGTTA TTAGTGGTTT ATCAGCAAA	1728
AAGTCCAATT TTAATTTAGT AAATGTTATC TTATACGTCA CAATAAAAAC ATTGCCTTTG	1788
AATGTTAATT TTTTGGTACA AAAGTCGACG GCCGC	1823

Figure 1 (continued)

Gln Met Asp Pro Asn Arg Ile Ser Glu Asp Gly Thr His Cys Ile Tyr  
 1 5 10 15

Arg Ile Leu Arg Leu His Glu Asn Ala Asp Phe Gln Asp Thr Thr Leu  
 20 25 30

Glu Ser Gln Asp Thr Lys Leu Ile Pro Asp Ser Cys Arg Arg Ile Lys  
 35 40 45

Gln Ala Phe Gln Gly Ala Val Gln Lys Glu Leu Gln His Ile Val Gly  
 50 55 60

Ser Gln His Ile Arg Ala Glu Lys Ala Met Val Asp Gly Ser Trp Leu  
 65 70 75 80

Asp Leu Ala Lys Arg Ser Lys Leu Glu Ala Gln Pro Phe Ala His Leu  
 85 90 95

Thr Ile Asn Ala Thr Asp Ile Pro Ser Gly Ser His Lys Val Ser Leu  
 100 105 110

Ser Ser Trp Tyr His Asp Arg Gly Trp Gly Lys Ile Ser Asn Met Thr  
 115 120 125

Phe Ser Asn Gly Lys Leu Ile Val Asn Gln Asp Gly Phe Tyr Tyr Leu  
 130 135 140

Tyr Ala Asn Ile Cys Phe Arg His His Glu Thr Ser Gly Asp Leu Ala  
 145 150 155 160

Thr Glu Tyr Leu Gln Leu Met Val Tyr Val Thr Lys Thr Ser Ile Lys  
 165 170 175

Ile Pro Ser Ser His Thr Leu Met Lys Gly Gly Ser Thr Lys Tyr Trp  
 180 185 190

Ser Gly Asn Ser Glu Phe His Phe Tyr Ser Ile Asn Val Gly Gly Phe  
 195 200 205

Phe Lys Leu Arg Ser Gly Glu Glu Ile Ser Ile Glu Val Ser Asn Pro  
 210 215 220

Ser Leu Leu Asp Pro Asp Gln Asp Ala Thr Tyr Phe Gly Ala Phe Lys  
 225 230 235 240

Val Arg Asp Ile Asp \*  
 245

Figure 2

CCCACGTCCC	GGGGAGCCAC	TGCCAGGACC	TTTGTGAACC	GGTCGGGGCG	GGGGCCGTGG	60
CGGAGTCTGC	TCGGCGGTGG	GTGGCCCGAG	AAGGGAGAGA	ACGATCGCGG	AGCAGGGCGC	120
CCGAACCTCCG	GGCGCCGCGC	C ATG CGC CGG GCC AGC CGA GAC TAC GGC AAG	Met Arg Arg Ala Ser Arg Asp Tyr Gly Lys			171
		250		255		
TAC CTG CGC AGC TCG GAA GAG ATG GGC AGC GGC CCC GGC GTC CCA CAC						219
Tyr Leu Arg Ser Ser Glu Glu Met Gly Ser Gly Pro Gly Val Pro His						
260	265	270				
GAA GGT CCG CTG CAC CCC GCG CCT TCT GCA CCG GCT CCG GCG CCG CCA						267
Glu Gly Pro Leu His Pro Ala Pro Ser Ala Pro Ala Pro Ala Pro Pro						
275	280	285				
CCC GCC GCC TCC CGC TCC ATG TTC CTG GCC CTC CTG GGG CTG GGA CTG						315
Pro Ala Ala Ser Arg Ser Met Phe Leu Ala Leu Leu Gly Leu Gly Leu						
290	295	300				
GGC CAG GTG GTC TGC AGC ATC GCT CTG TTC CTG TAC TTT CGA GCG CAG						363
Gly Gln Val Val Cys Ser Ile Ala Leu Phe Leu Tyr Phe Arg Ala Gln						
305	310	315		320		
ATG GAT CCT AAC AGA ATA TCA GAA GAC AGC ACT CAC TGC TTT TAT AGA						411
Met Asp Pro Asn Arg Ile Ser Glu Asp Ser Thr His Cys Phe Tyr Arg						
325	330	335				
ATC CTG AGA CTC CAT GAA AAC GCA GGT TTG CAG GAC TCG ACT CTG GAG						459
Ile Leu Arg Leu His Glu Asn Ala Gly Leu Gln Asp Ser Thr Leu Glu						
340	345	350				
AGT GAA GAC ACA CTA CCT GAC TCC TGC AGG AGG ATG AAA CAA GCC TTT						507
Ser Glu Asp Thr Leu Pro Asp Ser Cys Arg Arg Met Lys Gln Ala Phe						
355	360	365				
CAG GGG GCC GTG CAG AAG GAA CTG CAA CAC ATT GTG GGG CCA CAG CGC						555
Gln Gly Ala Val Gln Lys Glu Leu Gln His Ile Val Gly Pro Gln Arg						
370	375	380				
TTC TCA GGA GCT CCA GCT ATG ATG GAA GGC TCA TGG TTG GAT GTG GCC						603
Phe Ser Gly Ala Pro Ala Met Met Glu Gly Ser Trp Leu Asp Val Ala						
385	390	395	400			
CAG CGA GGC AAG CCT GAG GCC CAG CCA TTT GCA CAC CTC ACC ATC AAT						651
Gln Arg Gly Lys Pro Glu Ala Gln Pro Phe Ala His Leu Thr Ile Asn						
405	410	415				
GCT GCC AGC ATC CCA TCG GGT TCC CAT AAA GTC ACT CTG TCC TCT TGG						699
Ala Ala Ser Ile Pro Ser Gly Ser His Lys Val Thr Leu Ser Ser Trp						
420	425	430				
TAC CAC GAT CGA GGC TGG GCC AAG ATC TCT AAC ATG ACG TTA AGC AAC						747
Tyr His Asp Arg Gly Trp Ala Lys Ile Ser Asn Met Thr Leu Ser Asn						
435	440	445				
GGA AAA CTA AGG GTT AAC CAA GAT GGC TTC TAT TAC CTG TAC GCC AAC						795
Gly Lys Leu Arg Val Asn Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn						
450	455	460				
ATT TGC TTT CGG CAT CAT GAA ACA TCG GGA AGC GTA CCT ACA GAC TAT						843
Ile Cys Phe Arg His His Glu Thr Ser Gly Ser Val Pro Thr Asp Tyr						
465	470	475	480			

Figure 3

CTT CAG CTG ATG GTG TAT GTC GTT AAA ACC AGC ATC AAA ATC CCA AGT Leu Gln Leu Met Val Tyr Val Val Lys Thr Ser Ile Lys Ile Pro Ser 485 490 495	891
TCT CAT AAC CTG ATG AAA GGA GGG AGC ACG AAA AAC TGG TCG GGC AAT Ser His Asn Leu Met Lys Gly Gly Ser Thr Lys Asn Trp Ser Gly Asn 500 505 510	939
TCT GAA TTC CAC TTT TAT TCC ATA AAT GTT GGG GGA TTT TTC AAG CTC Ser Glu Phe His Phe Tyr Ser Ile Asn Val Gly Gly Phe Phe Lys Leu 515 520 525	987
CGA GCT GGT GAA GAA ATT AGC ATT CAG GTG TCC AAC CCT TCC CTG CTG Arg Ala Gly Glu Ile Ser Ile Gln Val Ser Asn Pro Ser Leu Leu 530 535 540	1035
GAT CCG GAT CAA GAT GCG ACG TAC TTT GGG GCT TTC AAA GTT CAG GAC Asp Pro Asp Gln Asp Ala Thr Tyr Phe Gly Ala Phe Lys Val Gln Asp 545 550 555 560	1083
ATA GAC TGA GACTCATTC GTGAAACATT AGCATGGATG TCCTAGATGT Ile Asp *	1132
TTGAAACTT CTTAAAAAAT GGATGATGTC TATACATGTG TAAGACTACT AAGAGACATG GCCACGGTG TATGAAACTC ACAGCCCTCT CTCTTGAGCC CTGTACAGGT TGTGTATATG TAAAGTCCAT AGGTGATGTT AGATTCATGG TGATTACACA ACGGTTTAC AATTTGTAA TGATTCCTA GAATTGAACC AGATTGGGAG AGGTATTCCG ATGCTTATGA AAAACTTACA CGTGAGCTAT GGAAGGGGGT CACAGTCTCT GGTCTAACCC CTGGACATGT GCCACTGAGA ACCTTGAAAT TAAGAGGATG CCATGTCATT GCATAGAAAT GATAGTGTGA AGGGTTAAGT TCTTTGAAT TGTTACATTG CGCTGGGACC TGCAAATAAG TTCTTTTTT CTAATGAGGA GAAAAATATA TGTATTTTTA TATAATGTCT AAAGTTATAT TTCAAGGTGTA ATGTTTTCTG TGCAAAGTT TGTAAATTAT ATTTGTGCTA TAGTATTGTA TTCAAAATAT TTAAAAATGT CTCACTGTTG ACATATTTAA TGTTTTAAAT GTACAGATGT ATTTAACTGG TGCACTTTGT AATTCCCTG AAGGTACTCG TAGCTAAGGG GGCAGAATAC TGTTCTGGT GACCACATGT AGTTTATTTC TTATTTCTTT TTAACCTAAT AGAGTCTTCA GACTTGTCAA AACTATGCAA GCAAAATAAA TAAATAAAA TAAAATGAAT ACCTTGAATA ATAAGTAGGA TGTTGGTCAC CAGGTGCCCT TCAAATTAG AAGCTAATTG ACTTTAGGAG CTGACATAGC CAAAAAGGAA CATAATAGGC TACTGAAATC TGTCAGGAGT ATTTATGCAA TTATTGAACA GGTGTCTTT TTTACAAGAG CTACAAATTG TAAATTGTTG TTCTTTTTT TTCCCATAGA AAATGTACTA TAGTTTATCA GCCAAAAAAC AATCCACTT TTAATTAGT GAAAGTTATT TTATTATACT GTACAATAAA AGCATTGTCT CTGAATGTTA ATTTTTGGT ACAAAAAATA AATTGTACG AAAAAAAAA AAAAAAAA AAAAA	1192 1252 1312 1372 1432 1492 1552 1612 1672 1732 1792 1852 1912 1972 2032 2092 2152 2212 2237

Figure 3 (continued)

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Met	Arg	Arg	Ala	Ser	Arg	Asp	Tyr	Gly	Lys	Tyr	Leu	Arg	Ser	Ser	Glu
1					5				10					15	
Glu	Met	Gly	Ser	Gly	Pro	Gly	Val	Pro	His	Glu	Gly	Pro	Leu	His	Pro
	20						25						30		
Ala	Pro	Ser	Ala	Pro	Ala	Pro	Ala	Pro	Pro	Pro	Ala	Ala	Ser	Arg	Ser
	35						40						45		
Met	Phe	Leu	Ala	Leu	Leu	Gly	Leu	Gly	Gln	Val	Val	Cys	Ser		
	50					55			60						
Ile	Ala	Leu	Phe	Leu	Tyr	Phe	Arg	Ala	Gln	Met	Asp	Pro	Asn	Arg	Ile
	65					70			75					80	
Ser	Glu	Asp	Ser	Thr	His	Cys	Phe	Tyr	Arg	Ile	Leu	Arg	Leu	His	Glu
	85							90					95		
Asn	Ala	Gly	Leu	Gln	Asp	Ser	Thr	Leu	Glu	Ser	Glu	Asp	Thr	Leu	Pro
	100							105					110		
Asp	Ser	Cys	Arg	Arg	Met	Lys	Gln	Ala	Phe	Gln	Gly	Ala	Val	Gln	Lys
	115					120							125		
Glu	Leu	Gln	His	Ile	Val	Gly	Pro	Gln	Arg	Phe	Ser	Gly	Ala	Pro	Ala
	130					135			140						
Met	Met	Glu	Gly	Ser	Trp	Leu	Asp	Val	Ala	Gln	Arg	Gly	Lys	Pro	Glu
	145					150			155					160	
Ala	Gln	Pro	Phe	Ala	His	Leu	Thr	Ile	Asn	Ala	Ala	Ser	Ile	Pro	Ser
	165							170					175		
Gly	Ser	His	Lys	Val	Thr	Leu	Ser	Ser	Trp	Tyr	His	Asp	Arg	Gly	Trp
	180					185							190		
Ala	Lys	Ile	Ser	Asn	Met	Thr	Leu	Ser	Asn	Gly	Lys	Leu	Arg	Val	Asn
	195						200					205			
Gln	Asp	Gly	Phe	Tyr	Tyr	Leu	Tyr	Ala	Asn	Ile	Cys	Phe	Arg	His	His
	210					215			220						
Glu	Thr	Ser	Gly	Ser	Val	Pro	Thr	Asp	Tyr	Leu	Gln	Leu	Met	Val	Tyr
	225					230			235				240		
Val	Val	Lys	Thr	Ser	Ile	Lys	Ile	Pro	Ser	Ser	His	Asn	Leu	Met	Lys
	245					250							255		
Gly	Gly	Ser	Thr	Lys	Asn	Trp	Ser	Gly	Asn	Ser	Glu	Phe	His	Phe	Tyr
	260					265							270		
Ser	Ile	Asn	Val	Gly	Gly	Phe	Phe	Lys	Leu	Arg	Ala	Gly	Glu	Glu	Ile
	275					280							285		
Ser	Ile	Gln	Val	Ser	Asn	Pro	Ser	Leu	Leu	Asp	Pro	Asp	Gln	Asp	Ala
	290					295			300						
Thr	Tyr	Phe	Gly	Ala	Phe	Lys	Val	Gln	Asp	Ile	Asp	*			
	305					310			315						

Figure 4

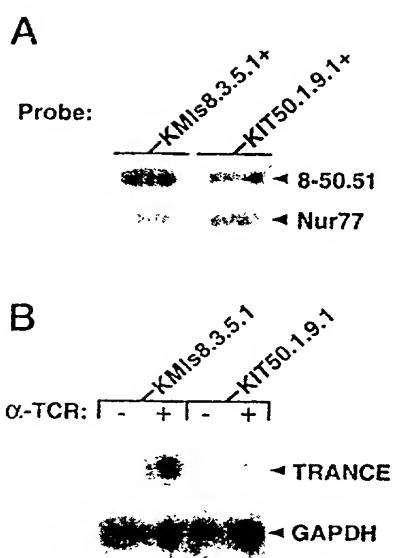


Figure 5

A

1 MRRAASRDYCKYLRGSIENRGPGVPHIGLTHPAPAPAPAPPAAGRSMFLALLGLGLGQ mTRANCE  
61 VVCGLALCFLYERAQMDPNRISEDSTHCFYRLRHNENAGLQDSTLESRUT--LPDSCRIM mTRANCE  
.....G.....J.....DF.....T.....O.....KLI.....I hTRANCE  
119 KQAFQAVVKEIQLHIVGDPQPSGADAMMEEGCGWLDVQAORGKPEAQPFHATINAASIPSGS mTRANCE  
.....S.....HTRAEK..VD.....L.....K.....S.....L.....TD..... hTRANCE  
179 IKVTHGQWYIINDRGWARTSNMTI.SNGKLRLVNQFGFYLYANICFRHIIETGGSVPTDYLQLM mTRANCE  
.....S.....G.....F.....I.....D.....A.....E..... hTRANCE  
239 YVYVVKTSIQLPGSHINLMKGJSTKNWSKINSEFIIYYSINVGGFFKLRAAEKLSIQVSNPSLL mTRANCE  
.....T.....T.....Y.....S.....E..... hTRANCE  
299 DIPPOQATYECAPKVQDID 316  
.....R..... mTRANCE  
.....R..... hTRANCE

B

Figure 6

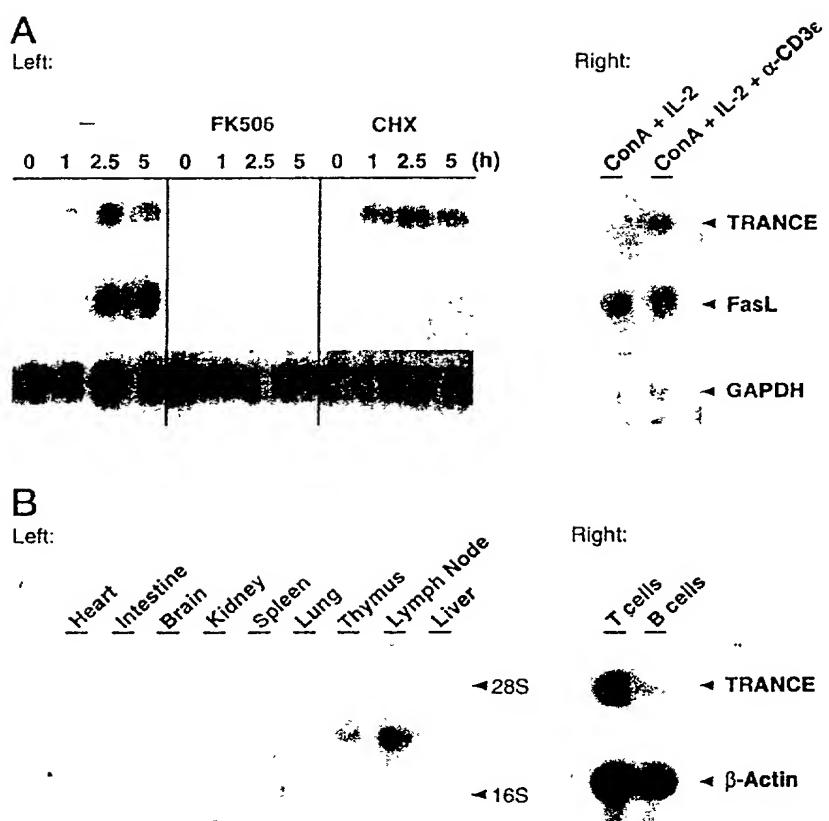


Figure 7

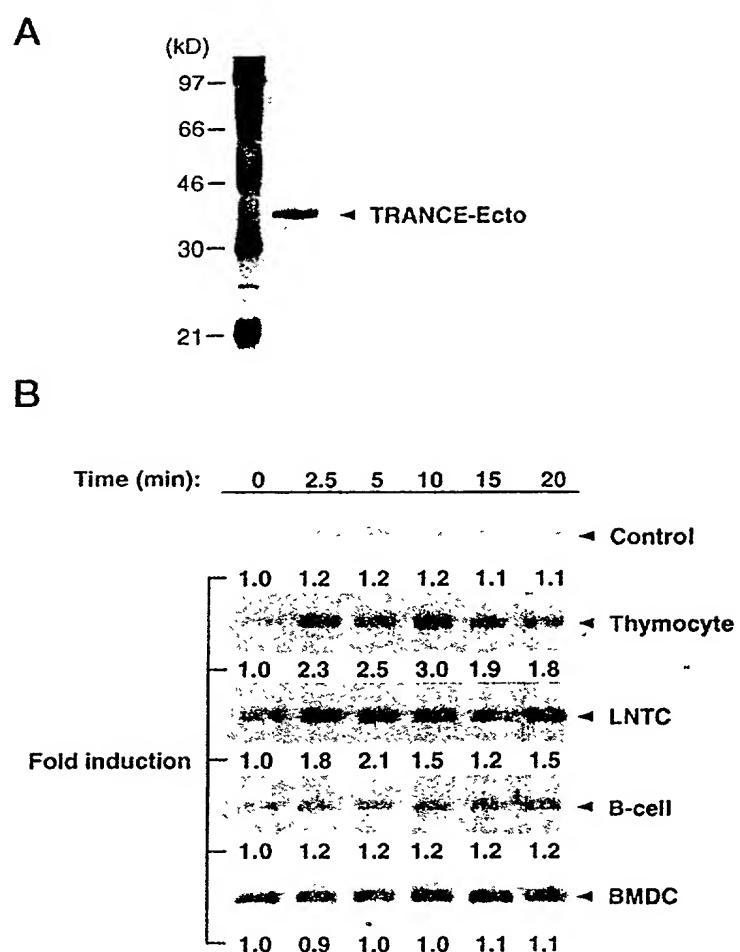


Figure 8

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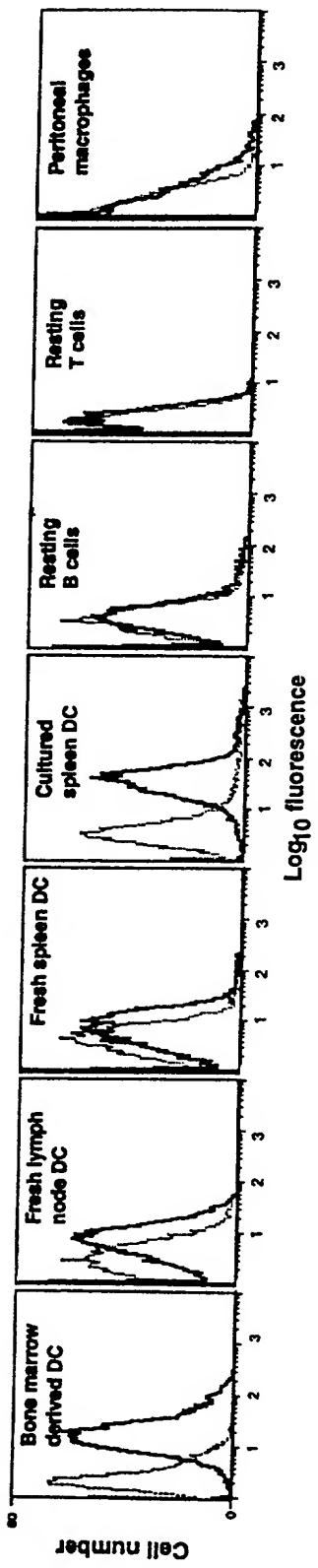


Figure 9

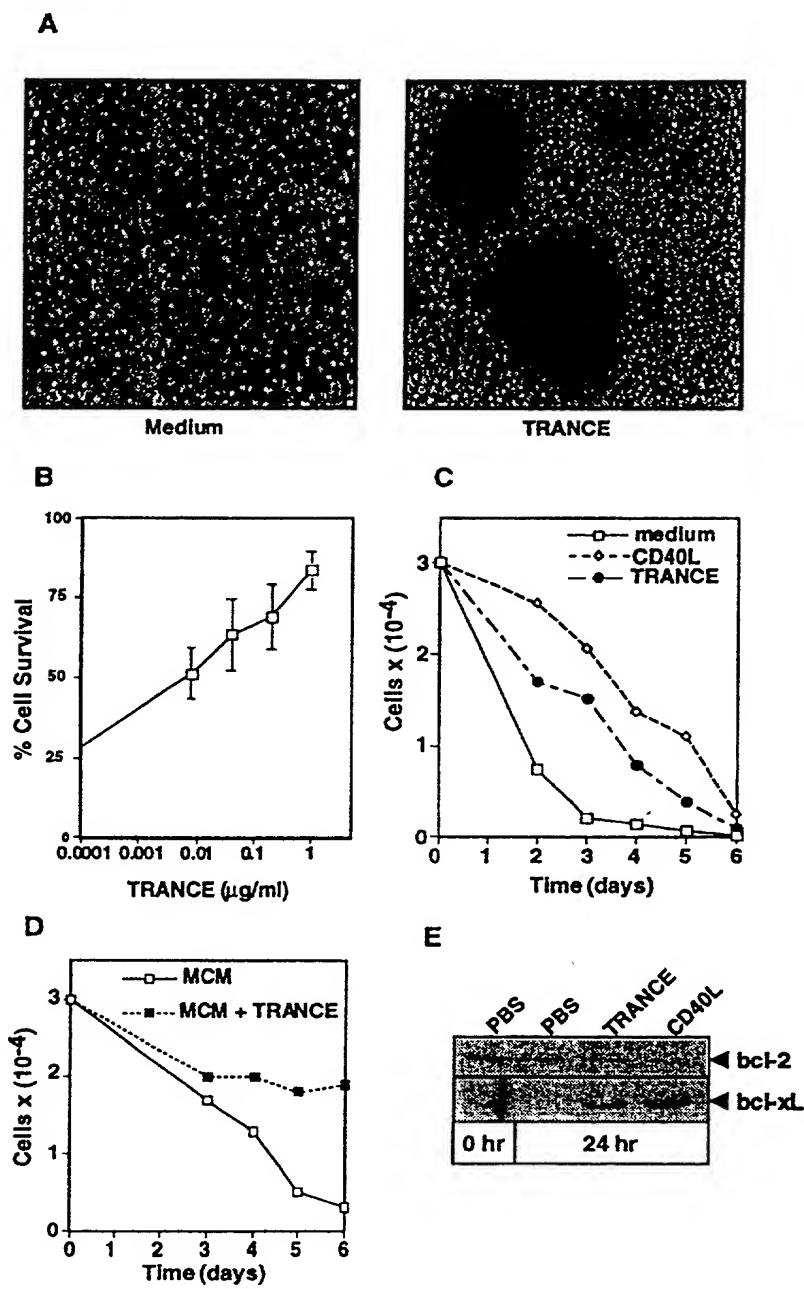


Figure 10

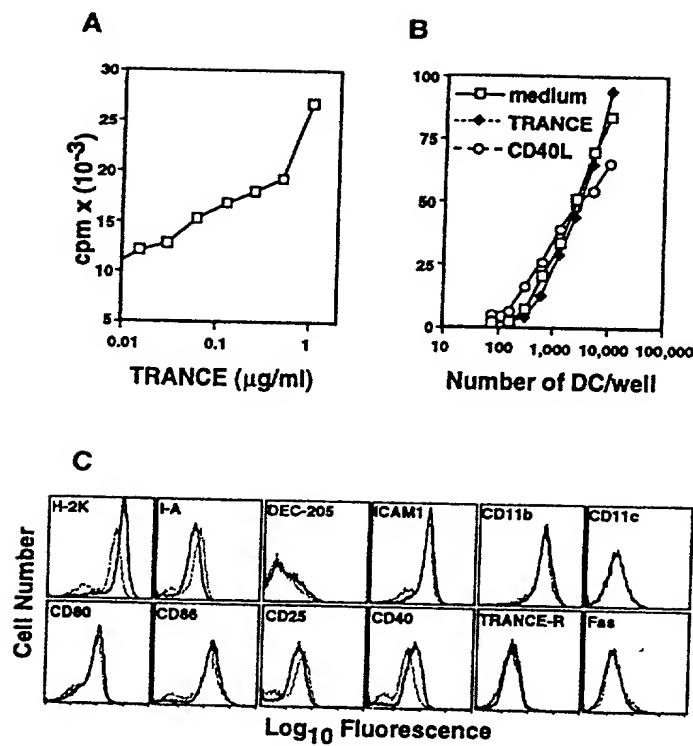


Figure 11

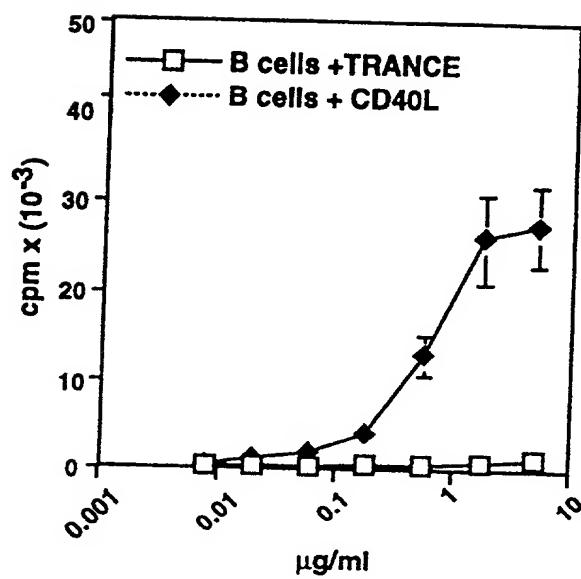


Figure 12

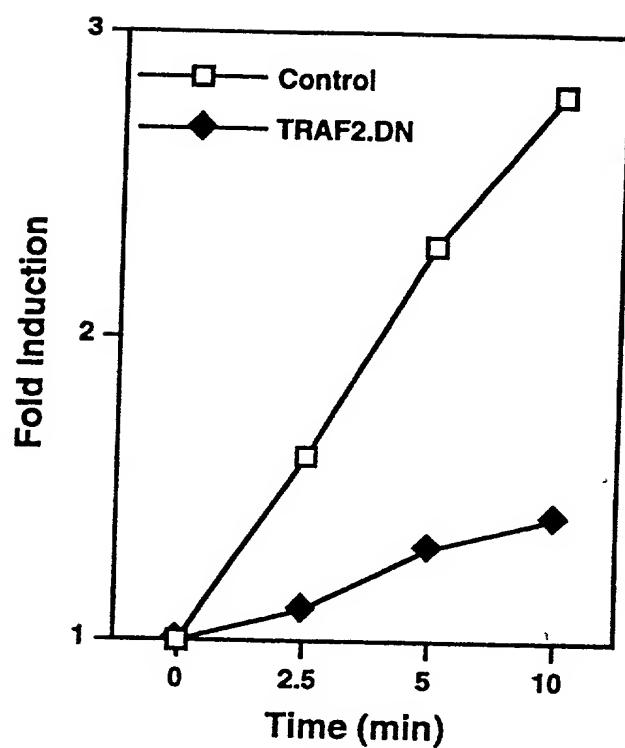


Figure 13